

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/576,684  
Source: FWP  
Date Processed by STIC: 5/1/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/576,684

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4   J   Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence.  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10   J   Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11   J   Use of <220>     Sequence(s) 1,2,7,8 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."  
                    Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/576,684

DATE: 05/01/2006  
TIME: 09:50:13

Input Set : A:\pto.da.txt  
Output Set: N:\CRF4\05012006\J576684.raw

*see pp 1-5*

3 <110> APPLICANT: c-LEcta GmbH  
W--> 4 <120> TITLE OF INVENTION: Method for the selection of biomolecules from biomolecule  
variant  
W--> 5 libraries  
W--> 6 <130> FILE REFERENCE: 401P03DPCT  
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/576,684  
C--> 8 <141> CURRENT FILING DATE: 2006-04-20  
8 <150> PRIOR APPLICATION NUMBER: DE10350474.5  
9 <151> PRIOR FILING DATE: 2003-10-23  
11 <160> NUMBER OF SEQ ID NOS: 11  
12 <170> SOFTWARE: PatentIn version 3.3

*see item 4 on Error  
summary  
sheet*

## ERRORED SEQUENCES

**Does Not Comply  
Corrected Diskette Needed**

552 <210> SEQ ID NO: 10  
E--> 553 <211> *← mandatory response needed*  
554 <212> TYPE: DNA  
555 <213> ORGANISM: artificial  
W--> 556 <220> FEATURE:  
557 <223> OTHER INFORMATION: substrate "Sub\_G" *give source of genetic material*  
W--> 558 <220> FEATURE:  
559 <223> OTHER INFORMATION: the g at position 24 is a ribonucleotide *(see item 11 on Error summary sheet)*  
W--> 560 <400> SEQUENCE: 10  
E--> 561 ccataccagc cagccacaag caagccaccg aagcacagat a  
565 <210> SEQ ID NO: 11  
E--> 566 <211> *← mandatory response needed*  
567 <212> TYPE: DNA  
568 <213> ORGANISM: artificial  
W--> 569 <220> FEATURE:  
570 <223> OTHER INFORMATION: substrate "Sub\_A" *same error as above*  
W--> 571 <220> FEATURE:  
572 <223> OTHER INFORMATION: the a at position 24 is a ribonucleotide  
W--> 573 <400> SEQUENCE: 11  
574 ccataccagc cagccacaag caaaccaccg aagcacagat a  
E--> 581 <sup>①</sup> *delete*

*see following pages for more errors*

10/576,684

2

<210> 1

<211> 28

<212> DNA

<213> artificial

<400> 1

caattctgca gttgcgttca cgtcgttg

*need explanation*

*(see item 11 on*

28

*Error summary sheet)*

<210> 2

<211> 28

<212> DNA

<213> artificial

<400> 2

taaggctcat gaaaaacaca gctatcgc

28

*same error in*

*Seqs. 7-8*

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3

<210> 5  
<211> 7336  
<212> DNA  
<213> Plasmid pA2T1  
<220>  
<221> lac promotor  
<222> (1)..(371)<223>

invalid response. See item 10 on Error  
summary  
sheet

same error in sequence 6

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<210> 9  
<211> 98  
<212> DNA  
<213> artificial  
<220>  
<223> Primer Loop1\_32

see p.5

Per Sequence Rules

all n's need to be explained in (2207-223) section

<220>  
<223> compositions of n and b are further specified in the description  
<400> 9

(invalid response)

gtaggatcca attcttacc acacnnbnnb nnbnnbnnbn nbnnbnnbnn bnnbnnbnnb

60

nnbnnbnnbn nbnnbgaatg gcctatcctc tcgagcgg

98

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/576,684

DATE: 05/01/2006

TIME: 09:50:15

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\05012006\J576684.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:9; N Pos. 25,26,28,29,31,32,34,35,37,38,40,41,43,44,46,47,49,50,52,53

Seq#:9; N Pos. 55,56,58,59,61,62,64,65,67,68,70,71,73,74

6

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/576,684

DATE: 05/01/2006

TIME: 09:50:15

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\05012006\J576684.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier  
L:6 M:283 W: Missing Blank Line separator, <130> field identifier  
L:8 M:270 C: Current Application Number differs, Replaced Current Application No  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:19 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>  
ORGANISM:artificial  
L:19 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>  
ORGANISM:artificial  
L:19 M:283 W: Missing Blank Line separator, <400> field identifier  
L:19 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:19  
L:27 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>  
ORGANISM:artificial  
L:27 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>  
ORGANISM:artificial  
L:27 M:283 W: Missing Blank Line separator, <400> field identifier  
L:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:27  
L:35 M:283 W: Missing Blank Line separator, <220> field identifier  
L:36 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:39 M:283 W: Missing Blank Line separator, <220> field identifier  
L:40 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:43 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:38  
L:43 M:283 W: Missing Blank Line separator, <400> field identifier  
L:43 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:42  
L:65 M:283 W: Missing Blank Line separator, <220> field identifier  
L:66 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:69 M:283 W: Missing Blank Line separator, <220> field identifier  
L:70 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:73 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:68  
L:73 M:283 W: Missing Blank Line separator, <400> field identifier  
L:73 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:72  
L:93 M:283 W: Missing Blank Line separator, <220> field identifier  
L:94 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:96 M:283 W: Missing Blank Line separator, <220> field identifier  
L:97 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:100 M:283 W: Missing Blank Line separator, <220> field identifier  
L:101 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:104 M:283 W: Missing Blank Line separator, <220> field identifier  
L:104 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:99  
L:105 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:108 M:283 W: Missing Blank Line separator, <220> field identifier  
L:108 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:103  
L:109 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:112 M:283 W: Missing Blank Line separator, <220> field identifier  
L:112 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:107  
L:113 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:116 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:111  
L:116 M:283 W: Missing Blank Line separator, <400> field identifier  
L:116 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:115  
L:371 M:283 W: Missing Blank Line separator, <220> field identifier  
L:372 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:375 M:283 W: Missing Blank Line separator, <220> field identifier  
L:376 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/576,684

DATE: 05/01/2006

TIME: 09:50:15

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\05012006\J576684.raw

L:379 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:379 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:374  
 L:380 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
 L:383 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:383 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:378  
 L:384 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
 L:387 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:387 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:382  
 L:388 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
 L:391 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:391 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:386  
 L:392 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
 L:395 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:390  
 L:395 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:395 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:394  
 L:524 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>  
 ORGANISM:artificial  
 L:524 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>  
 ORGANISM:artificial  
 L:524 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:524 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:524  
 L:533 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>  
 ORGANISM:artificial  
 L:533 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>  
 ORGANISM:artificial  
 L:533 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:533 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:533  
 L:541 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:543 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:545 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:546 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9  
 L:546 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9  
 L:546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
 L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:60  
 L:553 M:210 E: (40) Invalid Number of Sequences, LENGTH:  
 L:556 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:558 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:560 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:561 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:41 SEQ:10  
 L:566 M:210 E: (40) Invalid Number of Sequences, LENGTH:  
 L:569 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:571 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:573 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:581 M:254 E: No. of Bases conflict, this line has no nucleotides.  
 L:581 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:41 SEQ:11